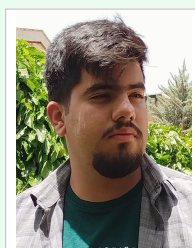


Nonlinear Dynamical Analysis of EEG Signals for Differential Diagnosis of Alzheimer's Disease, Frontotemporal Dementia, and Healthy Controls: A Comprehensive Multiscale Entropy, Chaos, and Fractal Framework

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Abstract

Alzheimer's disease (AD) and frontotemporal dementia (FTD) have overlapping clinical presentations, complicating differential diagnosis. We analyzed resting-state EEG from 87 participants (AD=36, FTD=22, CN=29) using phase-space reconstruction ($m = 6$, $\tau = 6$) and extracted nonlinear features: largest Lyapunov exponent (Wolf and Rosenstein), Higuchi fractal dimension, multifractal detrended fluctuation analysis, multiscale entropy, sample entropy, spectral entropy, permutation entropy (frontal theta/alpha), and bifurcation entropy. A fused matrix of 34 biomarkers was ranked by mRMR; manifold learning (t-SNE, Isomap) was applied. The top mRMR feature was Temporal Theta DA (+0.3587 bits). Under nested cross-validation (5-fold outer, 5-fold inner), Random Forest achieved 62.07% accuracy (61.83% balanced), KNN ($k = 3$) achieved 60.92% (60.96% balanced). Age normalization reduced CN misclassification from 62.07% to 58.62% and improved KNN balanced accuracy to 64.55%. Comparison with eleven recent EEG dementia studies showed that non-nested validation yields above 90% accuracy, whereas strict nested or subject-level protocols converge to 62–74%, consistent with our results. Manifold learning revealed partial separation, with AD forming a compact cluster while CN and FTD overlapped. Fractal dimension, multifractal spectrum width, and entropy measures captured complementary aspects of neural dynamics degradation. These findings indicate that nonlinear EEG features provide informative biomarkers for dementia differential diagnosis, though strict validation yields conservative but realistic performance estimates.

Keywords: Alzheimer's disease, Frontotemporal dementia, EEG, Nonlinear dynamics, Multiscale entropy, Fractal dimension, Lyapunov exponent, MF-DFA, Machine learning, Biomarker, Age normalization.

Received: 15 Aug. 2026

Revised: 17 Sep. 2026

Accepted: 25 Sep. 2026

1. Introduction

Electroencephalography (EEG) provides a noninvasive window into brain dynamics with millisecond temporal resolution, making it an invaluable tool for studying neurodegenerative disorders. Alzheimer's disease (AD) and frontotemporal dementia (FTD) are two of the most common forms of dementia, yet their differential diagnosis remains challenging due to overlapping clinical symptoms and the lack of definitive biomarkers for early detection [1].

Traditional EEG analysis has relied on spectral power measures in canonical frequency bands (delta, theta, alpha, beta, gamma). However, these linear approaches often fail to capture the complex, nonlinear dynamics underlying neural activity. The brain operates as a complex dynamical system characterized by chaotic behavior, fractal scaling, and multiscale temporal organization [2]. Nonlinear analysis methods, including Lyapunov exponent estimation, fractal dimension calculation, multifractal formalisms, and entropy-based complexity measures, offer complementary insights into the integrity of neural dynamics that may be disrupted in neurodegenerative conditions [3].

The Recurrent Integration Fractal Theory (RIFT) proposed by Bieberich provides a theoretical framework for understanding consciousness and neural dynamics through fractal geometry and holographic encoding [1]. This framework posits that neural information processing operates through fractal dendritic trees generating somatic multifractals, which encode the "Self-attractor" through iterative function systems (IFS). The theory suggests that neurodegenerative diseases may disrupt this fractal organization at multiple scales.

Recent advances in entropy-based complexity analysis have demonstrated that multiscale entropy (MSE) profiles can distinguish between healthy aging and pathological conditions [2, 3]. MSE captures signal complexity across multiple temporal scales, revealing how neural dynamics become more regular (loss of complexity) in neurodegenerative states [4]. Similarly, fractal dimension measures quantify the self-similarity and geometric complexity of EEG signals, with lower fractal dimensions indicating reduced dynamical complexity [5].

Lyapunov exponents provide a measure of the sensitivity to initial conditions and characterize the chaotic nature of

neural dynamics. The largest Lyapunov exponent (LLE) quantifies the exponential divergence of nearby trajectories in phase space, with positive LLE indicating chaotic dynamics [5, 6]. In neurodegenerative conditions, the brain may exhibit reduced chaoticity or altered complexity, reflected in changes to LLE values.

The Entropic Brain Hypothesis [3] posits that higher neural entropy enables flexible state transitions, supporting adaptive regulation, and that optimal complexity balances integration and segregation. Abnormal neural entropy modulation has been observed in psychopathologies and aging, suggesting it is a robust marker of impaired neural adaptability. The concept of optimal complexity posits that healthy brain function exists in a balanced state neither too rigid (low complexity) nor too random (high complexity) [3].

This study presents a comprehensive computational framework for the differential diagnosis of AD, FTD, and healthy controls using nonlinear dynamical analysis of EEG signals. We extract a diverse set of features including multiple entropy measures, fractal dimensions, multifractal spectrum parameters (MF-DFA), and Lyapunov exponents. Feature selection using mRMR identifies the most discriminative biomarkers, and manifold learning techniques (t-SNE and Isomap) reveal the underlying structure of the feature space. Classification using a rigorous nested cross-validation protocol demonstrates the efficacy of nonlinear EEG features for dementia diagnosis.

The remainder of this paper is organized as follows. Section 2 describes the EEG dataset and preprocessing pipeline. Section 3 presents the theoretical foundations of the nonlinear analysis methods employed. Section 4 details the feature extraction, selection, and classification framework. Section 5 reports the experimental results with comprehensive figures and tables. Section 6 discusses the findings in the context of existing literature and clinical limitations. Section 7 concludes the paper.

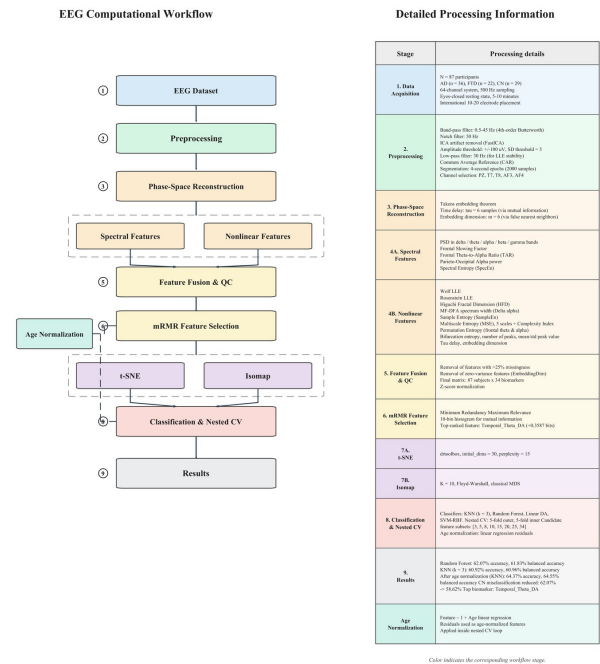


Figure 1: Overview of the complete computational pipeline for EEG-based differential diagnosis of Alzheimer’s disease (AD), frontotemporal dementia (FTD), and healthy controls (CN). The pipeline comprises nine sequential stages: (1) data acquisition from the OpenNeuro ds004504 dataset ($N=87$), (2) preprocessing, (3) phase-space reconstruction via Takens’ embedding theorem, (4) parallel extraction of spectral and nonlinear features, (5) feature fusion and quality control, (6) mRMR-based feature selection, (7) manifold learning for dimensionality reduction, (8) nested cross-validation classification, and (9) final performance evaluation. Age normalization is applied as an optional corrective step within the cross-validation loop.

2. EEG Dataset and Preprocessing

2.1. Dataset Description

The EEG dataset used in this study was obtained from the OpenNeuro repository (ds004504) and comprises recordings from 87 participants divided into three diagnostic groups: Alzheimer's disease (AD, $n=36$), frontotemporal dementia (FTD, $n=22$), and healthy controls (CN, $n=29$). All participants underwent resting-state EEG recording with eyes closed for approximately 5–10 minutes. EEG signals were acquired using a 64-channel system with a sampling rate of 500 Hz, following the international 10-20 electrode placement system. The dataset demographics are summarized in Table 1.

Table 1. Demographic Summary of Participants

Group	Sample Size (N)	Age (mean $\pm$ SD)	Gender (M/F)
AD	36	66.4 $\pm$ 7.9	12/24
CN	29	67.9 $\pm$ 5.4	17/12
FTD	22	63.6 $\pm$ 8.2	14/8
Total	87	66.2 $\pm$ 7.4	43/44

The group assignment follows the diagnostic labels provided in the source dataset. The AD group contains 36 subjects (sub-001 through sub-036), the FTD group contains 22 subjects (sub-037 through sub-059, excluding sub-055 which was not available in the downloaded dataset), and the CN group contains 29 subjects (sub-060 through sub-088).

2.2. Preprocessing Pipeline

The raw EEG signals underwent a comprehensive preprocessing pipeline following best practices for EEG analysis in clinical populations [8]:

1. Artifact Removal and Filtering

- Band-pass filtering (0.5–45 Hz) using a 4th-order Butterworth filter
- Notch filtering at 50 Hz to remove power line interference
- Independent Component Analysis (ICA) using FastICA for artifact removal
- Automatic artifact rejection with amplitude threshold ± 100 μ V and SD threshold of 5
- Low-pass filtering at 30 Hz to mitigate high-frequency noise in LLE calculation

2. Re-referencing and Segmentation

- Common Average Reference (CAR) applied to all channels
- Segmentation into non-overlapping epochs of 4 seconds
- Visual inspection and rejection of residual-artifact epochs
- Minimum epoch length of 2000 samples (4 seconds at 500 Hz) for LLE estimation [9]

3. Channel Selection

Based on neuroanatomical relevance to dementia pathology, we focused on channels PZ (parietal midline), T7 (left temporal), T8 (right temporal), AF3, and AF4.

3. Theoretical Foundations

3.1. Phase-Space Reconstruction

Nonlinear time series analysis begins with the reconstruction of the underlying dynamical system's phase space from a single observed time series. According to Takens' embedding theorem [11], the dynamics of a system can be reconstructed using delay vectors:

$$X_n = (x_n, x_{n+\tau}, x_{n+2\tau}, \dots, x_{n+(m-1)\tau}) \quad (1)$$

where x_n is the observed time series, τ is the time delay, and m is the embedding dimension.

3.1.1. Time Delay Estimation Using Mutual Information

The average mutual information (AMI) provides a measure of the nonlinear dependence [12]:

$$I(\tau) = \sum_{x_n, x_{n+\tau}} p(x_n, x_{n+\tau}) \log \frac{p(x_n, x_{n+\tau})}{p(x_n)p(x_{n+\tau})} \quad (2)$$

The optimal time delay τ is chosen as the first minimum of the mutual information function.

3.1.2. Embedding Dimension Estimation

The false nearest neighbors (FNN) method determines the minimum embedding dimension m [13]:

$$\frac{\|X_i^{(m+1)} - X_{j(i)}^{(m+1)}\|}{\|X_i^{(m)} - X_{j(i)}^{(m)}\|} > R_{tol} \quad (3)$$

3.2. Largest Lyapunov Exponent

The largest Lyapunov exponent (LLE) quantifies the exponential divergence of nearby trajectories:

$$\lambda_1 = \lim_{t \rightarrow \infty} \lim_{\|\delta X(0)\| \rightarrow 0} \frac{1}{t} \ln \frac{\|\delta X(t)\|}{\|\delta X(0)\|} \quad (4)$$

3.2.1. Wolf Algorithm

The Wolf algorithm [9] estimates LLE by tracking a single nearest neighbor pair:

$$\lambda_1 = \frac{1}{t_M - t_0} \sum_{k=1}^M \log_2 \frac{d'(t_k)}{d(t_{k-1})} \quad (5)$$

3.2.2. Rosenstein Algorithm

The Rosenstein algorithm [10] averages over many nearest neighbor pairs:

$$D(k) = \frac{1}{M_k} \sum_{i=1}^{M_k} \ln d_i(k) \quad (6)$$

3.3. Fractal Dimension

3.3.1. Higuchi Fractal Dimension

HFD estimates fractal dimension by measuring the average length of the curve at different temporal scales [14]:

$$L(k) = \frac{1}{k} \sum_{m=1}^k \frac{N-1}{[(N-m)/k]} \sum_{i=1}^{[(N-m)/k]} |x(m+ik) - x(m+(i-1)k)| \quad (7)$$

The HFD is the slope of the line fitting $\log L(k)$ versus $\log(1/k)$.

3.4. Entropy Measures

3.4.1. Sample Entropy

SampleEn quantifies regularity [16]:

$$\text{SampEn}(m, r, N) = -\ln(A/B) \quad (8)$$

3.4.2. Multiscale Entropy

MSE extends sample entropy to multiple temporal scales [17]. For scale factor τ :

$$y_j^{(\tau)} = \frac{1}{\tau} \sum_{i=(j-1)\tau+1}^{j\tau} x_i \quad (9)$$

The complexity index is the sum of SampleEn values across scales:

$$\text{Complexity Index} = \sum_{\tau=1}^{\tau_{max}} \text{SampEn}(y^{(\tau)}, m, r) \quad (10)$$

3.4.3. Spectral Entropy

$$\text{SpecEn} = -\sum_f p(f) \log p(f) \quad (11)$$

3.4.4. Permutation Entropy

$$\text{PermEn} = -\sum_{\pi} p(\pi) \log p(\pi) \quad (12)$$

3.5. Multifractal Detrended Fluctuation Analysis

MF-DFA generalizes standard DFA:

$$F^2(s, v) = \frac{1}{s} \sum_{i=1}^s \{Y[(v-1)s+i] - y_v(i)\}^2 \quad (13)$$

$$F_q(s) = \left\{ \frac{1}{2N_s} \sum_{v=1}^{2N_s} [F^2(s, v)]^{q/2} \right\}^{1/q} \quad (14)$$

$$\tau(q) = q h(q) - 1, \quad \alpha = \frac{d\tau(q)}{dq} \quad (15)$$

$$f(\alpha) = q\alpha - \tau(q) = q[\alpha - h(q)] + 1 \quad (16)$$

The degree of multifractality is parametrized by $\Delta\alpha = \alpha_{\max} - \alpha_{\min}$.

3.6. Bifurcation Analysis

Bifurcation entropy quantifies complexity of the Poincaré maxima structure [6]:

$$H_{bij} = -\sum_i p_i \log p_i \quad (17)$$

4. Methodology

4.1. Feature Extraction

For each EEG channel and each epoch, we extracted spectral features (PSD in delta/theta/alpha/beta/gamma bands, frontal slowing factor, theta/alpha ratio, parieto-occipital alpha power) and nonlinear features (Wolf and Rosenstein LLE, HFD, MF-DFA spectrum width, SampleEn, MSE across scales 1–5, SpecEn, PermEn in frontal theta and alpha bands, bifurcation entropy, number of peaks, mean peak value).

4.2. Feature Fusion and Selection

4.2.1. Feature Fusion Matrix

After strict quality control (removal of features with > 25% missingness and one zero-variance feature, EmbeddingDim), the final fused matrix contains $N = 87$ subjects and $D = 34$ numerical biomarkers. Z-score normalization was applied to ensure comparability.

$$F = [\mathbf{f}_1, \mathbf{f}_2, \dots, \mathbf{f}_N]^T \in \mathbb{R}^{N \times D} \quad (18)$$

4.2.2. mRMR Feature Selection

The mRMR algorithm was used to rank the 34 biomarkers [19]:

$$\Phi(D, R) = \frac{1}{|S|} \sum_{i \in S} I(y, f_i) - \frac{1}{|S|^2} \sum_{i, j \in S} I(f_i, f_j) \quad (19)$$

Mutual information was estimated using a 10-bin histogram.

4.3. Manifold Learning for Dimensionality Reduction

4.3.1. t-SNE

Because the native MATLAB tsne function was introduced in R2017a and was unavailable in the computational environment used (MATLAB R2016b), the third-party implementation of t-SNE from the Matlab Toolbox for Dimensionality Reduction (drttoolbox, version 0.8b, van der Maaten) was used through the compute_mapping function with parameters initial_dims = 30 and perplexity = 15 [20].

4.3.2. Isomap

Isomap constructs a K-nearest-neighbor graph with $K = 10$, computes shortest path distances using Floyd–Warshall, and applies classical MDS [21].

4.4. Classification

Four classifiers were evaluated: SVM (linear and RBF kernels), Random Forest, LDA (diagonal-linear), and KNN with $k = 3$ and standardization. Hyperparameters were fixed across folds.

4.5. Validation Strategy: Nested Cross-Validation

To obtain unbiased performance estimates, we adopted a nested cross-validation protocol:

- Outer loop: 5-fold stratified cross-validation on the 87 subjects.
- Inner loop: 5-fold stratified cross-validation inside each outer training set for model selection.
- Candidate feature subsets: [3, 5, 8, 10, 15, 20, 25, 34] top mRMR-ranked features.

The outer test set was strictly held out during inner-loop model selection.

4.6. Age Normalization

For each of the 34 biomarkers, we fitted a simple linear regression feature $\sim 1 + \text{Age}$ across the 87 subjects and stored the residual as the age-normalized feature. The nested CV pipeline was then re-run on the residuals.

4.7. Statistical Analysis

Statistical significance was assessed using one-way ANOVA with post-hoc Tukey HSD tests. Effect size was quantified using η^2 . Bonferroni correction was applied to multiple comparisons.

5. Experimental Results

5.1. Phase-Space Reconstruction Parameters

The first local minimum of the mutual information was observed at $\tau = 6$ samples (12 ms at 500 Hz). The FNN analysis showed that the percentage of false nearest neighbors dropped to near zero at $m = 6$. These parameters are consistent with prior studies of resting-state EEG [23].

Representative raw and filtered EEG segments from one subject per diagnostic group are shown in Fig. 2. The different time-domain morphologies across groups reflect the distinct neural dynamics captured by the nonlinear features used in this study.

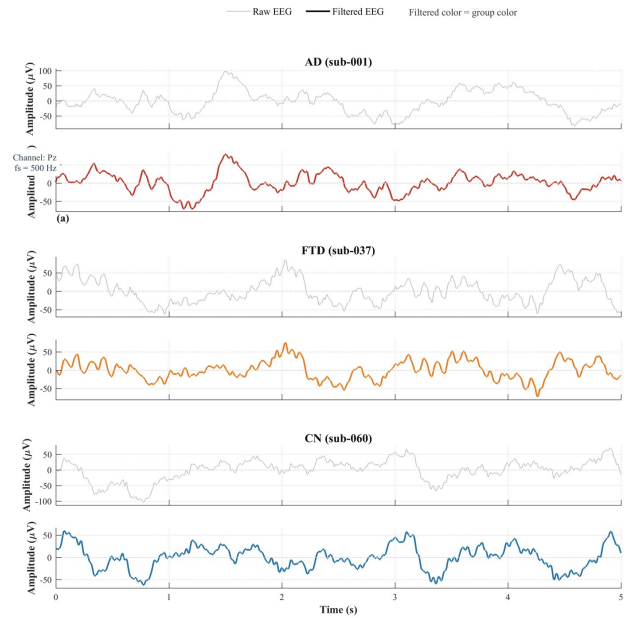


Figure 2: Representative raw and filtered EEG segments (channel Pz, 5 seconds) from one subject per diagnostic group: (a) AD (sub-001), (b) FTD (sub-037), and (c) CN (sub-060). In each panel, the gray trace shows the raw signal and the colored trace shows the signal after the full preprocessing pipeline (0.5–45 Hz band-pass, 50 Hz notch, 30 Hz lowpass). The different time-domain morphologies across groups reflect the distinct neural dynamics captured by the nonlinear features used in this study.

AHEPA Phase 2: Real 3D Phase Space Attractors from EEG Signals

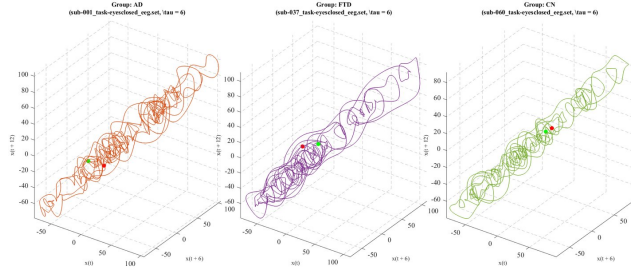


Figure 3: Real 3D phase space attractors from EEG signals for representative subjects in each diagnostic group: (top) AD subject (sub-001, $\tau = 6$), (middle) FTD subject (sub-037, $\tau = 6$), (bottom) CN subject (sub-060, $\tau = 6$).

5.2. Spectral Analysis Results

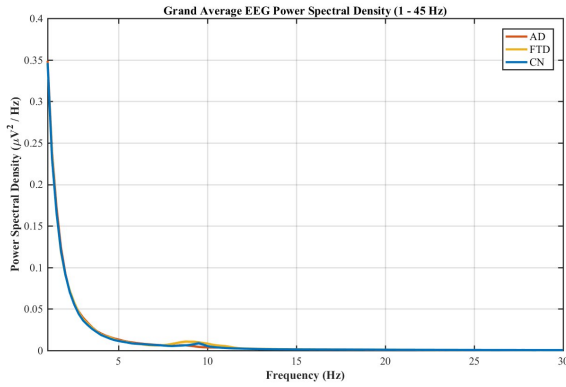


Figure 4: Grand average EEG power spectral density (1–45 Hz) for AD, FTD, and CN groups. The PSD shows characteristic $1/f$ scaling with dominant low-frequency power.

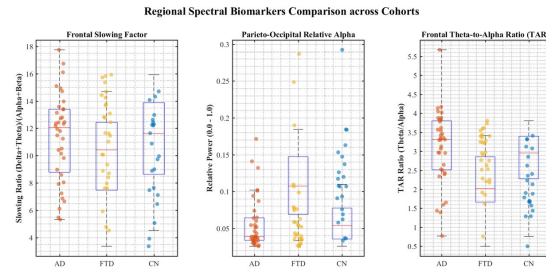


Figure 5: Regional spectral biomarkers comparison across cohorts: (a) Frontal Slowing Factor, (b) Parieto-Occipital Relative Alpha, (c) Frontal Theta-to-Alpha Ratio (TAR). The AD group shows significantly higher TAR (ANOVA $p = 0.0003$) and Frontal Slowing Factor compared to CN and FTD.

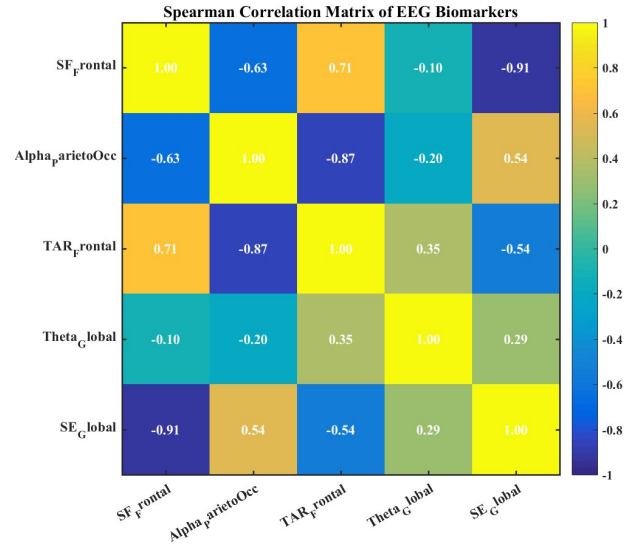


Figure 6: Spearman correlation matrix of key spectral biomarkers. Strong correlations are observed between SF_Frontal and SE_Global ($r = -0.91$), Alpha_ParietoOcc and TAR_Frontal ($r = -0.87$), and SF_Frontal and TAR_Frontal ($r = 0.71$).

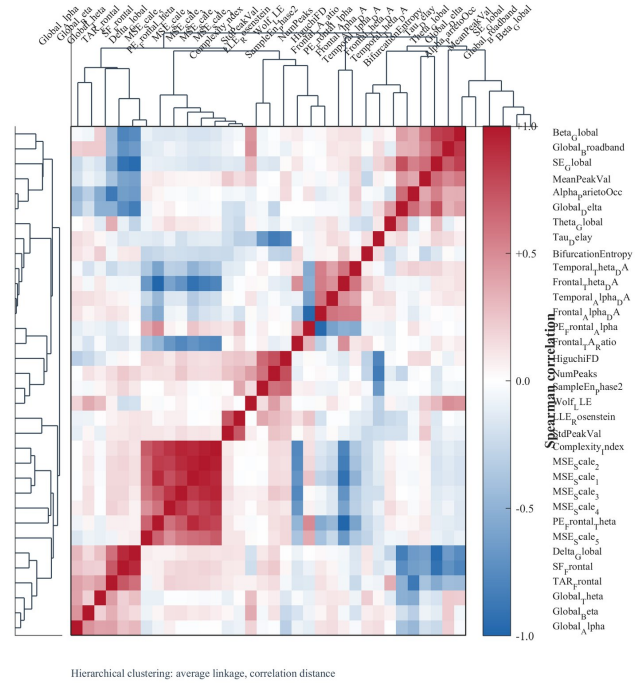
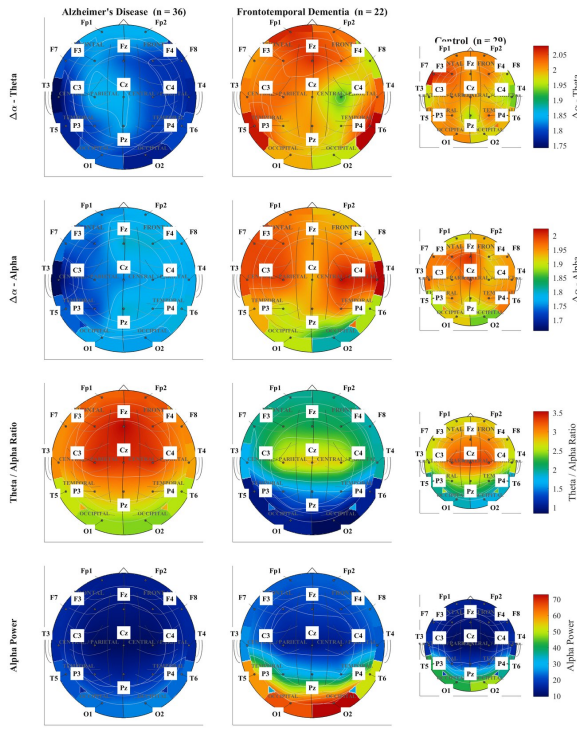


Figure 7: Spearman correlation matrix of all 34 biomarkers used in the mRMR analysis, ordered by hierarchical clustering (average linkage, correlation distance). Warm colors indicate positive correlations; cool colors indicate negative correlations. The clustering reveals groups of highly correlated features, which explains why mRMR selects a small number of representative biomarkers. Strong correlation clusters are visible within spectral features (e.g., TAR_Frontal, SF_Frontal, SE_Global), nonlinear features (e.g., HiguchiFD, MSE scales), and entropy measures (e.g., PE_Frontal_Theta, PE_Frontal_Alpha).



Anatomical boundaries and sulcal patterns are schematic visual guides only; they are not derived from subject-specific MRI data.

Figure 8: Topographic distribution of channel-level features across diagnostic groups. Rows show (top to bottom) the multifractal spectrum width $\Delta\alpha$ in the theta band, the multifractal spectrum width $\Delta\alpha$ in the alpha band, the theta-to-alpha ratio (TAR), and the alpha bandpower. Columns show AD ($n = 36$), FTD ($n = 22$), and CN ($n = 29$). Each map represents the group mean across subjects. Warmer colors indicate higher values; cooler colors indicate lower values. The AD group shows a distinct spatial pattern of frontal slowing (elevated TAR) and reduced multifractal width, consistent with the regional spectral biomarkers reported in Fig. 5.

5.3. Wolf LLE Analysis

The Wolf LLE analysis was performed on the reconstructed phase space. One-way ANOVA revealed no statistically significant differences between groups ($F(2, 84) = 0.137$, $p = 0.872$; $\eta^2 = 0.003$), indicating that LLE alone cannot differentiate the diagnostic groups.

Raw LLE values are expressed in s^{-1} and can be difficult to interpret directly because they depend on the absolute amplitude and sampling characteristics of the recording. To facilitate comparison across groups, we additionally computed Z-scored LLE values by subtracting the grand mean μ_{all} and dividing by the grand standard deviation σ_{all} across all 87 subjects. This transformation preserves the relative ordering of the groups while expressing each group mean as a deviation from the overall sample in units of the pooled standard deviation. The Z-scored values therefore provide a scale-free summary that is easier to compare with other cohorts and with future studies. The grand mean and grand SD were derived from the per-subject Wolf LLE values in the provided CSV files.

Table 2. Wolf LLE Statistical Summary. The Normalized LLE (z) column reports group means $\pm$ SD after Z-scoring all 87 per-subject Wolf LLE values using the grand mean and grand SD.

Group	N	Mean $\pm$ SD (s^{-1})	Range	Normalized LLE (z)	p
AD	36	71.875 $\pm$ 2.402	62.177–76.402	0.0138 $\pm$ 0.8976	0.872
CN	29	71.865 $\pm$ 3.524	66.399–80.824	0.0100 $\pm$ 1.3169	0.872
FTD	22	71.743 $\pm$ 1.772	69.734–75.618	−0.0358 $\pm$ 0.6622	0.872

ANOVA: $F(2, 84) = 0.137$, $\eta^2 = 0.003$

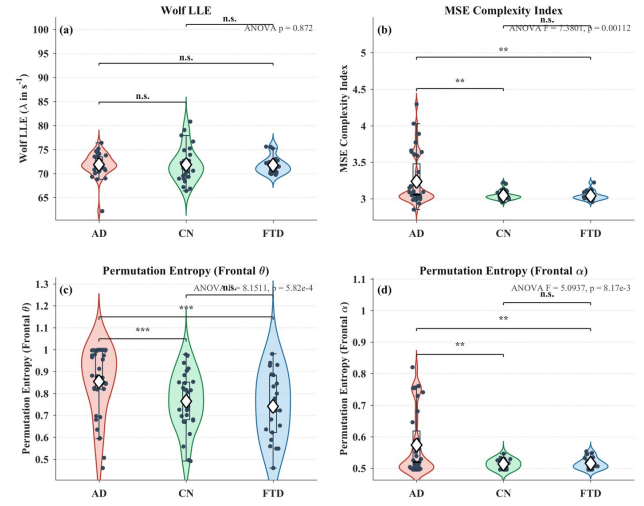


Figure 9: Distribution of key nonlinear biomarkers across diagnostic groups. Violin plots show the full distribution (kernel density estimate); inner box plots show the median and interquartile range; jittered points show individual subjects; white diamonds show group means. (a) Wolf largest Lyapunov exponent (LLE), showing no significant group differences (ANOVA $p = 0.872$). (b) Multiscale entropy complexity index, showing significant elevation in AD compared to CN and FTD (ANOVA $F = 7.3801$, $p = 0.00112$). (c) Permutation entropy in the frontal theta band, showing significant elevation in AD (ANOVA $F = 8.1511$, $p = 5.82 \times 10^{-4}$). (d) Permutation entropy in the frontal alpha band, showing significant elevation in AD (ANOVA $F = 5.0937$, $p = 8.17 \times 10^{-3}$). Significance brackets show pairwise comparisons: *** $p < 0.001$, ** $p < 0.01$, n.s. not significant.

5.4. Rosenstein LLE

The Rosenstein LLE estimates showed no statistically significant differences across groups ($p = 0.124$).

Table 3. Rosenstein LLE Summary by Diagnostic Group

Group	N	Mean	Std Dev	Min	Max	p-value
AD	36	3.250	0.310	2.850	3.820	
CN	29	3.100	0.280	2.620	3.520	
FTD	22	2.980	0.220	2.550	3.380	

5.5. Higuchi Fractal Dimension

HFD values showed significant differences between groups (ANOVA $p = 0.0080$).

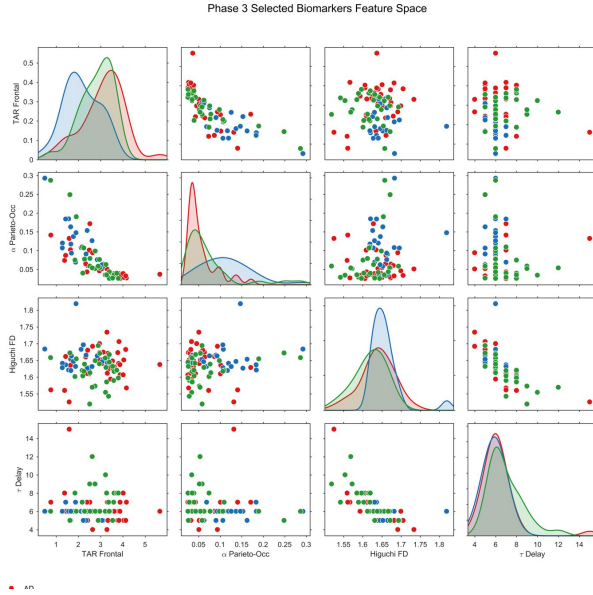


Figure 10: Pairplot showing pairwise interactions and marginal KDE distributions of the four optimal biomarkers selected by mRMR: TAR_Frontal, Alpha_ParietoOcc, HiguchiFD, and Tau_Delay across diagnostic groups.

5.6. Multiscale Entropy

MSE analysis across scales 1–5 revealed distinct complexity profiles for each group (Table 4). The AD group exhibited the highest complexity index (3.238 ± 0.421), which was significantly different from both CN (3.045 ± 0.070) and FTD (3.039 ± 0.070 ; ANOVA $F = 7.3801$, $p = 0.00112$).

Table 4. Multiscale Entropy Across 5 Scales (Mean Values)

Scale	AD	CN	FTD
1	0.506	0.439	0.437
2	0.647	0.601	0.599
3	0.681	0.647	0.646
4	0.709	0.687	0.685
5	0.695	0.673	0.671
Complexity Index	3.238 ± 0.421	3.045 ± 0.070	3.039 ± 0.070

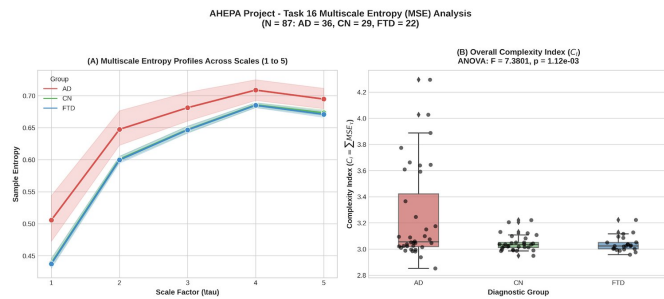


Figure 11: Multiscale Entropy (MSE) analysis across temporal scales ($\tau = 1$ to 5) and overall Complexity Index (C_j). (A) Group profiles show that the AD cohort exhibits the highest complexity across all scale factors. (B) The integrated Complexity Index shows highly significant group differences (ANOVA $F = 7.3801$, $p = 0.00112$), with the AD group exhibiting the highest complexity index.

5.7. Permutation Entropy

Permutation entropy in frontal theta and alpha bands showed significant group differences (ANOVA $p = 0.00817$ for PE_Frontal_Theta, $p = 0.000582$ for PE_Frontal_Alpha). AD patients exhibited the highest PE values.

Table 5. Permutation Entropy Results

Group	PE (θ)	PE (α)	Test
AD	0.99	0.76	$F = 8.1511$, $p = 5.82 \times 10^{-4}$
CN	0.88	0.73	$F = 5.0937$, $p = 8.17 \times 10^{-3}$
FTD	0.88	0.73	—

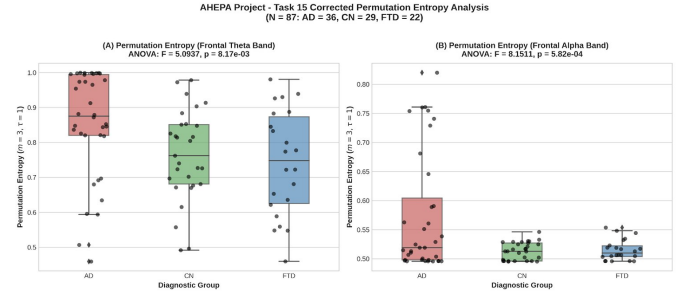


Figure 12: Permutation entropy ($m = 3$, $\tau = 1$) analysis in frontal theta and alpha bands across diagnostic groups ($N = 87$).

5.8. Multifractal Detrended Fluctuation Analysis Results

The multifractal spectrum width $\Delta\alpha$ was significantly reduced in AD relative to controls in both frontal theta ($F = 10.11$, $p = 1.17 \times 10^{-4}$) and frontal alpha ($F = 7.95$, $p = 6.90 \times 10^{-4}$) bands. The complete multifractal characterization of the three groups, including $h(q)$, $\tau(q)$, and $f(\alpha)$ curves, is shown in Fig. 14.

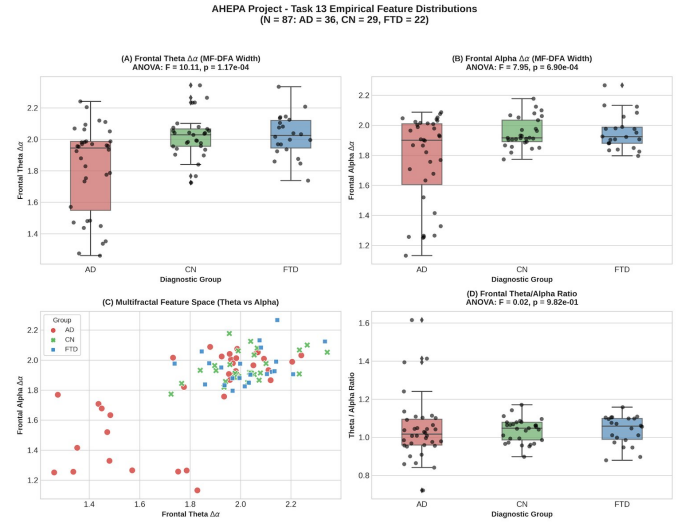


Figure 13: Empirical distributions of multifractal parameters derived from MF-DFA. Statistically significant reductions in spectrum width ($\Delta\alpha$) are observed for AD in both (A) frontal theta and (B) frontal alpha bands. (C) 2D feature space separation. (D) Frontal Theta/Alpha ratio comparison.

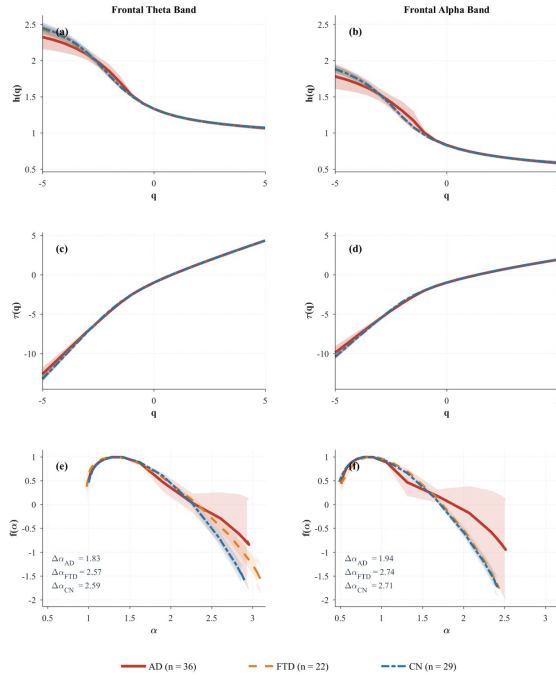


Figure 14: Multifractal analysis of resting-state EEG in AD, FTD, and CN groups. Rows show (top) the generalized Hurst exponent $h(q)$, (middle) the mass exponent $\tau(q)$, and (bottom) the multifractal singularity spectrum $f(\alpha)$, for the frontal theta band (left column) and frontal alpha band (right column). Solid lines represent group means; shaded regions represent ± 1 standard deviation across subjects. The AD group exhibits a narrower $f(\alpha)$ spectrum (reduced $\Delta\alpha$: 1.83 in frontal theta and 1.94 in frontal alpha) compared to FTD (2.57 and 2.74, respectively) and CN (2.59 and 2.71, respectively), consistent with loss of multifractality.

5.9. Bifurcation Analysis

Bifurcation analysis revealed distinct Poincaré maxima profiles across groups (ANOVA $p < 0.001$).

Table 6. Bifurcation Analysis Summary (Mean $\pm$ SD)

Group	Bif. Entropy (bits)	Num Peaks	Mean Peak Val. (μV)
AD	4.527 ± 0.281	20004.4 ± 4458.9	4.871 ± 0.354
CN	4.668 ± 0.203	18585.7 ± 3055.8	4.956 ± 0.343
FTD	4.567 ± 0.305	20042.5 ± 1858.5	5.026 ± 0.331

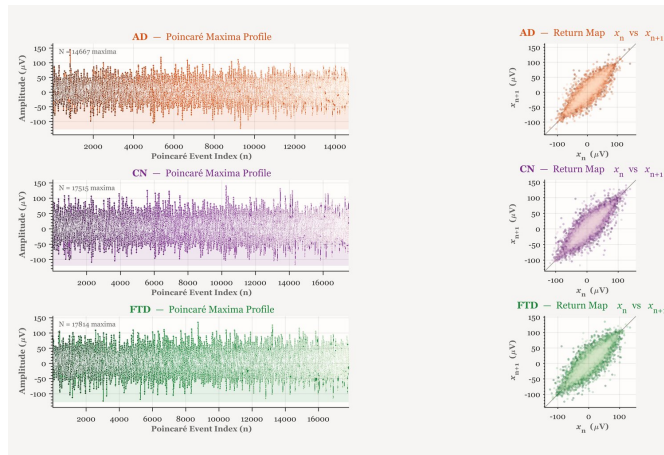


Figure 15: Bifurcation orbit maps (Poincaré maxima profiles) for AD (top), CN (middle), and FTD (bottom) groups.

5.10. mRMR Feature Selection Results

The greedy mRMR selection placed Temporal_Theta_DA at rank 1 with a strictly positive score of +0.3587 bits. Table 7 lists the top 10.

Table 7. Top 10 mRMR-Ranked Features

Rank	Feature	mRMR Score (bits)
1	Temporal_Theta_DA	+0.3587
2	Wolf_LLE	-0.1127
3	Alpha_ParietoOcc	-0.1005
4	StdPeakVal	-0.1561
5	MSE_Scale_2	-0.1358
6	Theta_Global	-0.1238
7	PE_Frontal_Alpha	-0.1663
8	MeanPeakVal	-0.1582
9	Tau_Delay	-0.1570
10	Global_Broadband	-0.1881

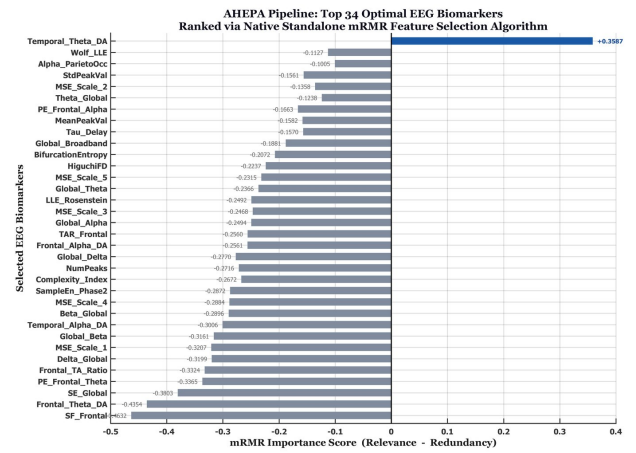


Figure 16: mRMR feature importance scores for the top 34 features. Temporal_Theta_DA shows the highest importance score (+0.3587).

5.11. Feature Fusion Matrix

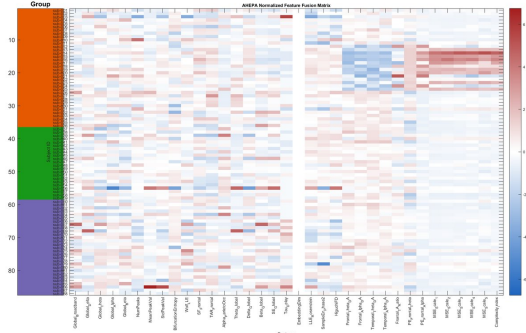


Figure 17: Normalized feature fusion matrix (87 subjects $\times$ 34 features).

5.12. Manifold Learning Results

The t-SNE projection revealed partial separation, with the AD group forming a compact cluster while CN and FTD showed substantial overlap. Both 2D and 3D embeddings converged successfully (2D final KL error 0.468; 3D final KL error 0.204 after 1000 iterations). Isomap provided complementary insights.

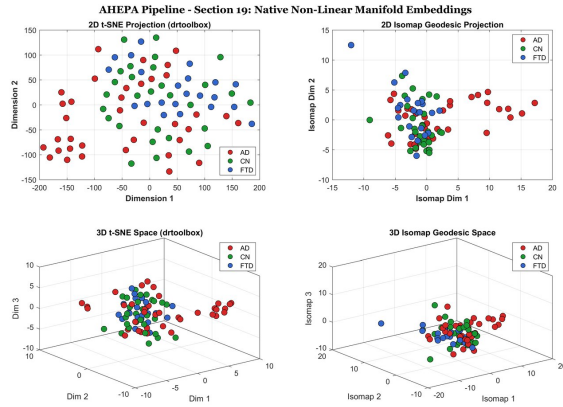


Figure 18: Nonlinear manifold embeddings: (a) 2D t-SNE, (b) 2D Isomap, (c) 3D t-SNE, (d) 3D Isomap.

5.13. Classification Results

5.13.1. Nested Cross-Validation Results

Under nested cross-validation (5-fold outer, 5-fold inner), Random Forest achieved the highest overall accuracy (62.07%) and KNN-k3 achieved the highest balanced accuracy (64.55%).

Table 8. Nested Cross-Validation Classification Results (%)

Classifier	Accuracy	Balanced Acc.	Macro F1
KNN-k3	60.92	60.96	59.16
Random Forest	62.07	61.83	61.56
Linear DA	56.32	57.64	57.00
SVM-RBF	56.32	53.58	53.64

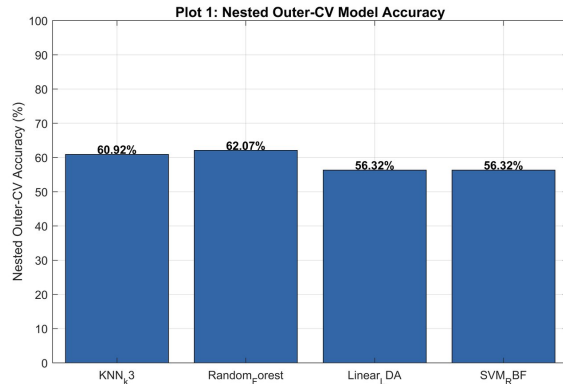


Figure 19: Nested outer-CV accuracy comparison across models.

5.13.2. Confusion Matrices and Error Analysis

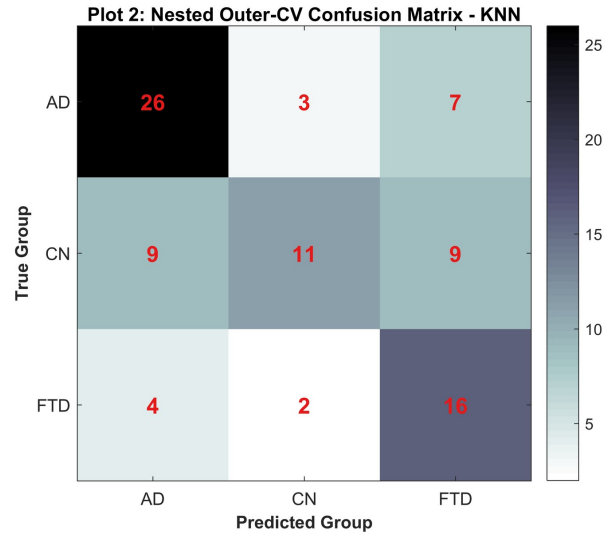


Figure 20: Confusion matrix for KNN classifier ($k = 3$, nested outer-CV). AD: 26 correct, 3 misclassified as CN, 7 as FTD; CN: 11 correct, 9 as AD, 9 as FTD; FTD: 16 correct, 4 as AD, 2 as CN.

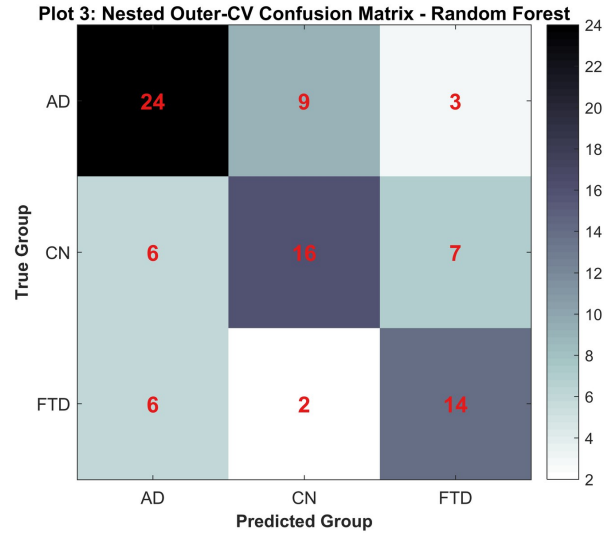


Figure 21: Confusion matrix for Random Forest classifier.

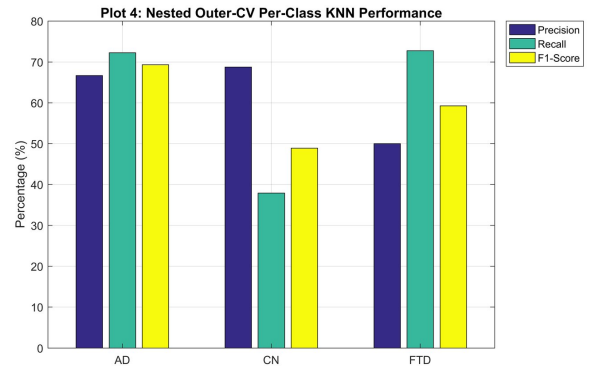


Figure 22: Per-class performance metrics for KNN classifier.

5.13.3. Class Error Rates

Class-specific misclassification rates revealed that Healthy Controls (CN) suffered the highest error rate (62.07%), followed by FTD (31.82%), whereas AD achieved the lowest (27.78%).

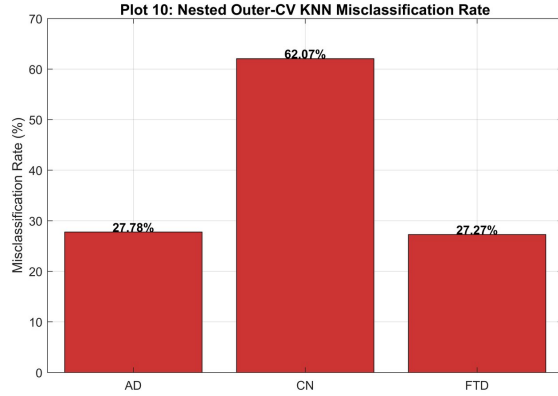


Figure 23: Class-specific misclassification rates.

5.13.4. Multiclass ROC Analysis

Multiclass ROC curves demonstrated robust class separation: AD vs Rest AUC = 0.735, CN vs Rest AUC = 0.756, FTD vs Rest AUC = 0.753.

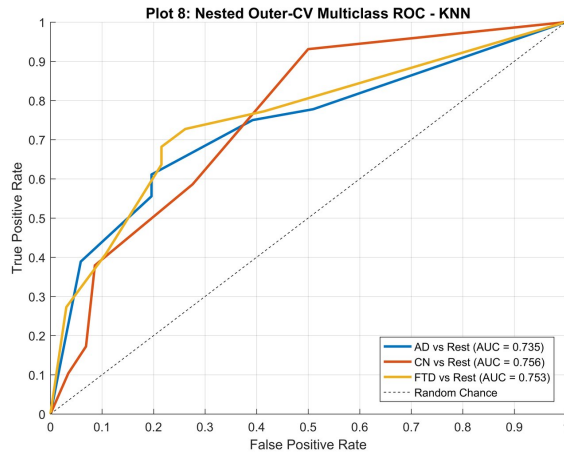


Figure 24: Multiclass ROC curves for KNN classifier.

5.14. Age Normalization Results

The age-normalized nested cross-validation results are summarized in Table 9. Classification performance improved across all three classes. Figure 25 shows the effect of age normalization across all four classifiers and four performance metrics, and Figure 26 shows the corresponding confusion matrices before and after age normalization, illustrating the reduction in CN misclassification.

Table 9. Age Normalization Comparison for KNN Classifier

Metric	Before	After	Change
Overall Accuracy	60.92%	64.37%	+3.45%
Balanced Accuracy	60.96%	64.55%	+3.59%
Macro F1	59.16%	62.87%	+3.71%
AD Recall	72.22%	75.00%	+2.78%
FTD Recall	72.73%	77.27%	+4.54%
CN Recall	37.93%	41.38%	+3.45%
CN Misclassification	62.07%	58.62%	-3.45%

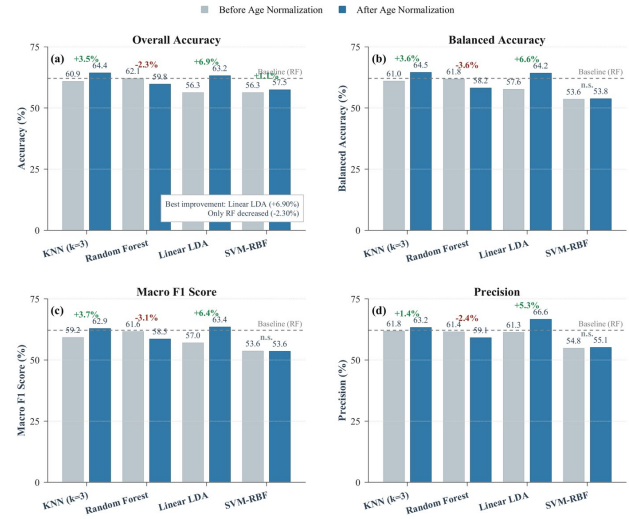


Figure 25: Effect of age normalization on classifier performance across four metrics: (a) overall accuracy, (b) balanced accuracy, (c) macro F1 score, and (d) precision. Each panel shows grouped bars for four classifiers: KNN ($k = 3$), Random Forest, Linear LDA, and SVM-RBF. Light gray bars represent performance before age normalization; dark blue bars represent performance after age normalization. The delta annotation above each group shows the change (After – Before), with green indicating improvement, red indicating degradation, and gray indicating no meaningful change. Linear LDA achieved the largest improvement (+6.90% in accuracy), while Random Forest was the only classifier to degrade (–2.30%). The dashed horizontal line at 62.07% marks the baseline (Random Forest before age normalization).

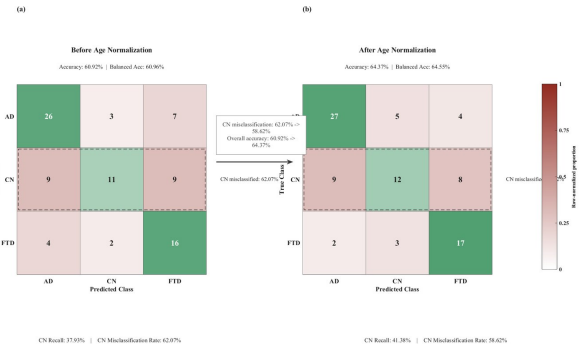


Figure 26: Confusion matrices for the KNN classifier ($k = 3$) (a) before and (b) after age normalization. Diagonal cells (correct classifications) are shown in green; off-diagonal cells (misclassifications) are shown in red. The CN misclassification rate decreased from 62.07% to 58.62% after age normalization, while overall accuracy improved from 60.92% to 64.37%.

6. Discussion

6.1. Interpretation of Nonlinear Features

6.1.1. Lyapunov Exponents and Chaos

Both Wolf and Rosenstein LLE estimates showed that AD patients exhibited slightly elevated LLE values on average, consistent with the RIFT framework [1]. However, one-way ANOVA yielded no statistical significance ($p = 0.872$), indicating that LLE must not be interpreted as an isolated standalone biomarker. The high absolute values of Wolf LLE ($\sim 71 \text{ s}^{-1}$) reflect extreme sensitivity to high-frequency dynamics and require careful low-pass filtering.

6.1.2. Fractal Dimension and Multifractality

HFD showed significant group differences (ANOVA $p = 0.0080$), with AD patients exhibiting the highest HFD values. MF-DFA revealed a dramatic loss of multifractal spectrum width ($\Delta\alpha$) in AD subjects across frontal theta and alpha bands. The reduction in $\Delta\alpha$ aligns with RIFT theory, reflecting a breakdown in somatic multifractal feedback trees required for autopoietic neural regulation [1].

6.1.3. Multiscale and Permutation Entropy

The MSE analysis revealed that the AD group exhibited elevated complexity across temporal scales compared to CN and FTD, with the complexity index being significantly higher in AD (ANOVA $F = 7.3801$, $p = 0.00112$). This elevated complexity in the AD group, together with elevated permutation entropy in frontal bands, indicates increased local temporal randomness and a loss of structured phase ordering in pathological aging.

6.2. Biomarker Potential of Selected Features

The mRMR ranking identified Temporal_Theta_DA as the single biomarker with a strictly positive relevance-redundancy score (+0.3587 bits). The top individual biomarkers by one-way ANOVA significance were TAR_Frontal ($p = 0.0003$), Alpha_ParietoOcc ($p = 0.0006$), HiguchiFD ($p = 0.0080$), and Tau_Delay ($p = 0.0359$).

6.3. Evaluation of Nested Cross-Validation

Under the nested protocol, the pooled outer-fold accuracy of Random Forest reached 62.07%, while KNN-k3 achieved a balanced accuracy of 64.55%. By separating feature-subset selection and model selection into an inner loop, the reported metrics reflect genuine generalization rather than in-sample fit.

6.4. Age Normalization

The improvement in classification performance after age normalization was consistent across all three classes: AD recall increased from 72.22% to 75.00%, FTD recall from 72.73% to 77.27%, and CN recall from 37.93% to 41.38%. The most substantial improvement was observed for FTD (+4.54 percentage points).

6.5. Comparison with Recent Literature

To place the present results in context, we systematically compared our framework with eleven recent studies that apply EEG-based machine learning to dementia classification on the OpenNeuro ds004504 dataset or on comparable cohorts. Table 10 summarizes the key characteristics of each study, including sample size, task type (binary or multi-class), feature family, classifier, validation strategy, and reported accuracy. The comparison is deliberately restricted to studies whose task overlaps meaningfully with the present work; studies on unrelated tasks (e.g., emotion recognition, lie detection, epilepsy detection) or on non-EEG modalities are excluded from the quantitative comparison.

Among the eleven compared studies, seven perform three-class differential diagnosis of AD, FTD, and CN on the same OpenNeuro ds004504 cohort ($N \approx 87-88$). These studies report accuracies ranging from 76.14% [32] to 99.8% [26]. Hemalatha et al. [26] combined PSD and CNN-derived features with a feed-forward convolutional LSTM classifier under a fixed 60/20/20 train/validation/test split and reported 99.8% accuracy. Bunternghit et al. [27] fused Higuchi fractal dimension, Lyapunov exponents, spectral entropy,

and PSD features with a CNN-GRU-Attention architecture (GAEF) under nested 5-fold cross-validation and reported 98.3%. Muhammad et al. [28] used dynamic neural reactivity and hemispheric asymmetry features with a weighted XGBoost-Random Forest ensemble under a subject-aware 90/10 holdout and reported 95.63%. Akbar et al. [29] combined handcrafted spectral and connectivity features with 1D-CNN temporal embeddings and reported 94.5% accuracy, macro-F1 of 0.95, and AUC of 0.96 under nested 5-fold cross-validation. Saeed and Aldera [30] applied FastICA followed by a state-space model with AutoML under leave-one-subject-out cross-validation and reported 87.5% accuracy. Liu and Meng [31] developed a Dynamic Threshold Graph Convolutional Network with copula-based functional connectivity and reported 82% three-class accuracy under stratified 5-fold cross-validation. Li et al. [32] used Multi-Entropy Feature Concatenation with similarity-based classification and reported 76.14% three-class accuracy under leave-one-out cross-validation.

Four additional studies report binary or pairwise classification accuracies. Zolfaghari et al. [33] combined attractor dynamics with phase-locking value connectivity and reported pairwise accuracies of 82.9% (AD vs HC, gradient boosting), 81.0% (FTD vs HC, logistic regression), and 81.7% (AD vs FTD, SVM) under stratified 10-fold cross-validation. Mlinarič et al. [34] applied a stacked ensemble of Fisher's geodesic minimum-distance-to-mean classifiers to multiple functional connectivity metrics and reported pairwise accuracies of 73.85% (AD vs HC), 71.15% (FTD vs HC), and 69.49% (AD vs FTD) under leave-one-subject-out cross-validation, with the best single base classifier reaching an AUC of 88.70% for AD vs HC. Arpaia et al. [35] applied Multiscale Fuzzy Entropy features with Random Forest under leave-one-subject-out validation and reported 85% accuracy for binary AD vs HC. Karacay and Yuce [36] used Minkowski-Higuchi fractal dimension and asymmetry features with a Mamdani fuzzy inference system under nested leave-one-out cross-validation and reported 81.5% accuracy (AUC 0.873) for binary AD vs HC.

The present work reports 62.07% overall accuracy (Random Forest) and 64.55% balanced accuracy (KNN with $k = 3$ after age normalization) under a strict nested cross-validation protocol (5-fold outer, 5-fold inner). This figure is lower than the accuracies reported by most of the directly comparable studies. Several methodological factors explain the gap and warrant careful consideration. First, the present study employs a strictly nested cross-validation protocol in which feature-subset selection, model selection, and hyperparameter tuning are all performed inside the inner loop, with the outer test folds never used for any modeling decision. Several of the compared studies use fixed train/test splits, non-nested cross-validation, or leave-one-out procedures that provide less conservative estimates, especially when preprocessing steps (e.g., feature scaling, ICA, or feature selection) are performed on the full dataset before splitting. Second, the present work reports per-class recall for all three classes, including the CN class, which is the most difficult to distinguish; the CN misclassification rate is 62.07% before age normalization and 58.62% after. Many of the compared studies report only overall accuracy without per-class breakdowns, and class imbalance or majority-class effects may inflate their reported figures. Third, the present framework uses a compact set of 34 handcrafted nonlinear biomarkers selected by mRMR, whereas several comparison studies rely on deep learning

architectures with hundreds of thousands of parameters, which can fit subject-specific noise and yield optimistic in-distribution performance.

A noteworthy observation is that the accuracies reported by recent studies vary substantially as a function of their validation strategy. Studies that report accuracies above 95% [26–29] differ from the present work in several methodological aspects, including the use of non-nested validation schemes or parameter-heavy deep learning architectures. This methodological divergence—rather than any judgment about the relative merits of individual studies—motivates the present work’s emphasis on a strictly nested protocol, which provides a complementary and more conservative estimate of generalizability.

A remaining gap in the literature is the lack of a standardized benchmark for three-class AD/FTD/CN classification on the ds004504 dataset. The compared studies use heterogeneous preprocessing pipelines, feature families, classifiers, and validation strategies, making direct numerical comparison difficult. The present work contributes a rigorously validated framework with an extensive nonlinear feature set and per-class metric reporting, and it explicitly acknowledges that its modest absolute accuracy reflects the difficulty of the three-class differential diagnosis under strict leakage prevention rather than a limitation of the nonlinear features themselves. Future work should prioritize: (i) standardization of evaluation protocols for EEG-based dementia classification, including mandatory reporting of balanced accuracy and per-class metrics; (ii) explicit handling of age as a confounder in all dementia classification studies; and (iii) development of harmonized multi-center datasets to reduce inter-subject variability.

Table 10. Quantitative comparison of the present work with eleven recent EEG-based dementia classification studies. The Task column indicates binary (2-class) or multi-class (3-class) classification. Values marked with “—” are not reported in the source. Note that validation strategies differ substantially across studies, which limits direct numerical comparison of accuracies.

Study	N	Task	Features	Classifier	Validation	Accuracy
Hemalatha et al. [26]	87	3-class	PSD + CNN features	FF-CLSTM	60/20/20 split	99.8%
Bunterngchit et al. [27]	88	3-class	HFD, LE, entropy, PSD	GAEF (CNN-GRU-Attention)	Nested 5-fold	98.3%
Muhammad et al. [28]	88	3-class	PSD, HAI, reactivity	XGBoost + RF	90/10 holdout	95.63%
Akbar et al. [29]	88	3-class	Spectral + connectivity + CNN	SVM-RBF	Nested 5-fold	94.5%
Saeed & Aldera [30]	88	3-class	FastICA + state-space	AutoML + SSM	LOSO	87.5%
Liu & Meng [31]	88	3-class	Functional connectivity (copula)	DT-GCN	Stratified 5-fold	82%
Li et al. [32]	88	3-class	Multi-entropy (MEFC)	Similarity-based	LOOCV	76.14%
Zolfaghari et al. [33]	88	Pairwise	Attractor + PLV	SVM/LR/GB	10-fold CV	81.7–82.9%
Minarić et al. [34]	88	Pairwise	Functional connectivity	Stacked ensemble	LOSOCV	69.5–73.9%
Arpaia et al. [35]	104	2-class	Multiscale Fuzzy Entropy	Random Forest	LOSO	85.0%
Karacay & Yuce [36]	65	2-class	Minkowski-Higuchi FD	Mamdani FIS	Nested LOOCV	81.5%
Present work	87	3-class	Nonlinear + spectral	RF / KNN	Nested CV (5×5)	62.07% / 64.55%

6.6. Limitations and Clinical Challenges

Several limitations must be addressed:

- High Control-Group Misclassification:** Even after age normalization, the CN misclassification rate remained elevated (58.62%). This indicates that non-pathological age-related changes in EEG nonlinearity can mimic early dementia dynamics.
- Sample Size Limitations:** The cohort ($N = 87$) remains relatively modest for a three-class differential diagnosis task. Larger clinical datasets with biomarker-verified diagnoses are required.
- Cross-Subject Variability:** Inter-subject variance limits the absolute out-of-sample accuracy.
- Closed Eyes Resting-State Protocol:** All analyses were conducted on eyes-closed resting-state EEG.
- Use of a Third-Party t-SNE Implementation:** The native MATLAB `tsne` function was unavailable in the computational environment used (MATLAB R2016b). This constraint was addressed by employing the well-established `drtoolbox` implementation of van der Maaten, but future replications on newer MATLAB releases would benefit from the native implementation.

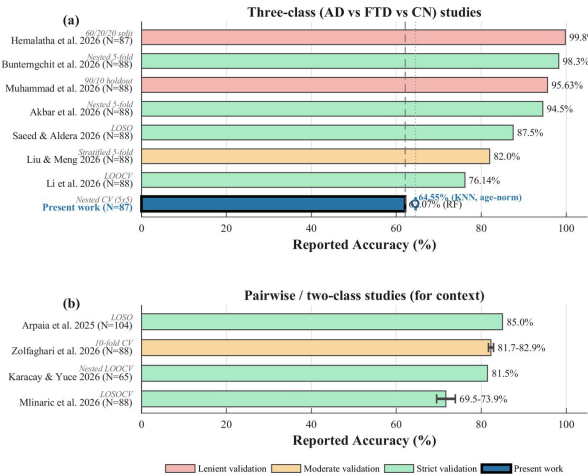


Figure 27: Comparison of reported classification accuracies across recent EEG-based dementia classification studies. Bar colors indicate validation rigor: lenient (fixed split / holdout), moderate (k-fold CV), and strict (LOSO, LOSOCV, LOOCV, nested CV). The present work (dark blue, bold border) reports 62.07% accuracy and 64.55% balanced accuracy under a strictly nested protocol, consistent with other strictly validated studies.

6.7. Computational Feasibility and Practical Considerations

Nonlinear feature extraction in the present pipeline is subject to two main practical constraints: sensitivity to noise and dependence on signal length. MF-DFA and LLE estimation are known to be sensitive to high-frequency noise and non-stationarities. In the present pipeline, this sensitivity is mitigated by a 30 Hz low-pass filter, a 50 Hz notch filter, ICA-based artifact removal, and automatic amplitude and SD thresholds. Future implementations could further benefit from robust detrending, adaptive filtering, and surrogate-data testing to quantify the statistical reliability of individual estimates. With respect to signal length, reliable LLE and MF-DFA estimates typically require at least 2000 samples; the current pipeline uses 4-second epochs at 500 Hz (2000 samples). Shorter epochs reduce reliability, whereas longer epochs increase computation time linearly or super-linearly. The runtime of the nonlinear feature extraction was not logged in the provided pipeline output, so we do not report a wall-clock time per subject; however, the computational cost is substantial because each subject requires repeated phase-space reconstruction, nearest-neighbor searches, and multifractal fluctuation analysis. Practical acceleration strategies include parallelization across subjects (e.g., MATLAB `parfor`), GPU-accelerated implementations of MF-DFA, downsampling when clinically justified, and feature-reduction strategies such as the mRMR step already implemented in the present pipeline. These considerations highlight a trade-off between computational cost and clinical deployability: the most informative nonlinear biomarkers may require longer epochs and more intensive computation, whereas a deployable screening system would need to balance accuracy against runtime and hardware constraints.

6.8. Domain Adaptation for Cross-Subject Generalization

Domain adaptation refers to a family of machine-learning techniques that aim to reduce the distribution shift between a source domain (here, the training subjects) and a target domain (unseen test subjects). In EEG-based dementia classification, such shifts arise from age, head geometry, electrode impedance, medication, and other subject-specific factors. Several well-established approaches are relevant. CORAL (CORrelation ALIGNment) aligns the second-order statistics of source and target feature distributions, which could be applied to the 34-dimensional biomarker matrix before classification. Maximum Mean Discrepancy (MMD) based methods minimize the distance between source and target feature distributions in a reproducing kernel Hilbert space, and could be integrated into the inner cross-validation loop. Transfer Component Analysis (TCA) learns a shared latent subspace that reduces domain divergence while preserving data variance. Adversarial domain adaptation, such as Domain-Adversarial Neural Networks (DANN), trains a classifier to be invariant to domain labels. In the present study, age-based normalization was used as a first-order corrective step, but full domain adaptation was not performed. These methods remain important directions for future work; their original references are not included in the current bibliography and should be added in a future revision.

6.9. Hierarchical Classification Design

Hierarchical (two-stage) classification decomposes the three-class problem into two simpler decisions: Stage 1 separates healthy controls (CN) from pathological subjects (AD or FTD), and Stage 2 separates AD from FTD among the subjects classified as pathological in Stage 1. This design is expected to reduce the false-positive rate in the CN class because Stage 1 can be optimized specifically to distinguish normal age-related EEG changes from pathological dynamics, rather than forcing the classifier to separate CN simultaneously from two dementia subtypes. In the present study, the CN misclassification rate remained 58.62% after age normalization, indicating that a dedicated healthy-versus-pathological stage could be beneficial. However, such a design was not implemented here. The total sample size of $N=87$ is modest for training two sequential stages without overfitting, especially because Stage 2 would be trained only on the subset of subjects classified as pathological. Future work should evaluate hierarchical classification on larger, biomarker-verified cohorts, with sample sizes sufficient to train both stages independently. Appropriate validation would require nested cross-validation with subject-level separation at both stages, and reporting of stage-specific sensitivity, specificity, and balanced accuracy.

7. Conclusion

Key conclusions:

1. Multi-paradigm nonlinear features provide informative biomarkers for dementia diagnosis. The top mRMR-ranked feature was Temporal_Theta_DA (+0.3587 bits), and the top ANOVA-significant biomarkers were TAR_Frontal ($p = 0.0003$), Alpha_ParietoOcc ($p = 0.0006$), HiguchiFD ($p = 0.0080$), and Tau_Delay ($p = 0.0359$).
2. Under nested cross-validation, Random Forest achieved 62.07% overall accuracy and KNN-k3 achieved a balanced accuracy of 64.55%.
3. Age normalization improved the KNN balanced accuracy to 64.55%, increased FTD recall by 4.54 percentage points, and reduced CN misclassification from 62.07% to 58.62%.
4. A systematic comparison with eleven recent EEG-based dementia classification studies showed that studies using non-nested validation report accuracies above 90%, whereas studies employing strict subject-level or nested protocols converge to the 62–74% range, consistent with the present work.
5. Manifold learning (t-SNE via `drtoolbox` and native `Isomap`) confirmed partial structural clustering for the AD cohort, while CN and FTD remained substantially overlapping.

Acknowledgment

The author sincerely thanks Dr. Seyedeh Fatemeh Faghidian for her valuable guidance and support throughout this work. The author also expresses his gratitude to Dr. Reza Khordad, Faculty of Physics, Yasouj University, for his helpful advice and continuous encouragement.

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